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PCTUS2004037793.seq.list.txt
SEQUENCE LISTING

<110> UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.

<120> DNA SEQUENCE AND EXPRESSED RECOMBINANT GLYCOPROTEINS
RELATED TO FELINE THYROTROPIN

<130> 235-00540201

<140> PCT/US04/03779

<141> 2004-11-12

<150> 60/534,205

<151> 2004-01-05

<150> 60/519,302

<151> 2003-11-12

<160> 18

<170> PatentIn Ver. 3.3

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35 40 45

Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
50 55 60

Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
65 70 75 80

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Arg Lys Glu²⁰ Cys Ala Tyr Cys Leu²⁵ Thr Ile Asn Thr Thr³⁰ Ile Cys Ala
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 Gly Tyr Cys Met Thr Arg Asp⁵⁵ Ile Asn Gly Lys Leu⁶⁰ Phe Leu Pro Lys
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 Tyr Ala Leu Ser Gln Asp⁷⁰ Val Cys Thr Tyr Arg⁷⁵ Asp Phe Leu Tyr Lys⁸⁰
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 Thr Val Glu Ile Pro⁸⁵ Gly Cys Pro His His⁹⁰ Val Thr Pro Tyr Phe⁹⁵ Ser
 85 90 95
 Tyr Pro Val Ala¹⁰⁰ Val Ser Cys Lys Cys¹⁰⁵ Gly Lys Cys Asn Thr¹¹⁰ Asp Tyr
 100 105 110
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 Met Gly Cys³⁵ Cys Phe Ser Arg Ala⁴⁰ Tyr Pro Thr Pro Ala⁴⁵ Arg Ser Lys
 35 40 45
 Lys Thr Met Leu Val Pro Lys⁵⁵ Asn Ile Thr Ser Glu⁶⁰ Ala Thr Cys Cys
 50 55 60
 Val Ala Lys Ala Phe Thr⁷⁰ Lys Ala Thr Val Met⁷⁵ Gly Asn Ala Lys Val⁸⁰
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Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala
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 Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
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 Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
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 35 40 45
 Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys Thr Val Glu Ile
 50 55 60
 Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser Tyr Pro Val Ala
 65 70 75 80
 Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr Ser Asp Cys Ile
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 100 105 110
 Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser Lys Ala Pro Ser
 115 120 125
 Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro Ser Asp Thr Pro
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 Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro
 145 150 155 160
 Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro
 165 170 175
 Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
 180 185 190
 Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr Ser Glu
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 65 70 75 80

Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
 85 90 95

Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
 100 105 110

Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
 115 120 125

Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser
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Gln Gly Cys Pro Glu Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys
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 195 200 205

Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 210 215 220

Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
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Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu
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agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct 144
Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala
35 40 45

gga tat tgt atg aca cgg gat atc aat ggc aaa ctg ttt ctt ccc aaa 192
Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
50 55 60

tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag 240
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
65 70 75 80

act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc 288
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser
85 90 95

tac ccg gta gct gta agc tgt aaa tgt ggc aag tgt aat act gac tat 336
Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr
100 105 110

agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc aaa ccc 384
Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr Lys Pro
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accatcaaca ccaccatctg tgctggatat tgtatgacac gggtatgtag ttcattctac 180
    
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ccctaggtta taatatacgg acctactcca tacagttggg acagataatt tttaacaatag 360
ttttactccc aaagttttatt taaaccttat cttgttccca cgatcaagga taaaagagag 420
gtgtgtgtgt atgtcattttt tttttgtctc tataggattc agtgtggata tgctgaattg 480
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gcgaattaac attttgcttc ctcttctgtg cttccctcag gatatacatg gcaaactgtt 600
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tgtagaaata ccaggatgcc cacaccatgt tactccctat ttctcctacc cggtagctgt 720
aagctgtaaa tgtggcaagt gtaatactga ctatagcgac tgcatacatg aggccatcaa 780
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aaggaaaaca aatacttctc caagttgggt gccccaattt atcaatgcat gggctgctgc 180
ttctccagag catacccccac tccagcaagg tccaagaaga caatgttggg cccaaagaac 240
atcacctcag aagccacatg ctgtgtggcc aaagccttta ccaaggccac ggtaatggga 300
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                                         Met Asp Tyr Tyr Arg
                                         1 5

aaa tat gca gct gtc att ctg gcc ata ctc tct gtg ttt ctg cat att 162
Lys Tyr Ala Ala Val Ile Leu Ala Ile Leu Ser Val Phe Leu His Ile
                        10 15 20

ctc cat tct ttt cct gat gga gag ttt aca atg cag ggg tgc cca gaa 210
Leu His Ser Phe Pro Asp Gly Glu Phe Thr Met Gln Gly Cys Pro Glu
                        25 30 35

tgc aag cta aag gaa aac aaa tac ttc tcc aag ttg ggt gcc cca att 258
Cys Lys Leu Lys Glu Asn Lys Tyr Phe Ser Lys Leu Gly Ala Pro Ile
                        40 45 50

tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc act cca gca 306
Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Ala

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70 75 80 85			
aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta atg gga aat	402		
Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val Met Gly Asn			
90 95 100			
gcc aaa gtg gag aat cac aca gag tgc cac tgc agc act tgc tat cac	450		
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Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His Val Glu			
20 25 30			
agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc tgt gct	144		
Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile Cys Ala			
35 40 45			
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Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys			
50 55 60			
tat gct ctg tcc caa gat gtt tgc acc tac aga gac ttc ctg tac aag	240		
Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys			
65 70 75 80			
act gta gaa ata cca gga tgc cca cac cat gtt act ccc tat ttc tcc	288		
Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr Phe Ser			
85 90 95			
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Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr Asp Tyr			
100 105 110			

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115 120 125	
cag aag tcc gat gtg gta gga gtt tct atc cag gac tcc tct tcc tca	432
Gln Lys Ser Asp Val Val Gly Val Ser Ile Gln Asp Ser Ser Ser Ser	
130 135 140	
aag gcc cct tcc gcc agc ctt cca agc cca acg cgt ctc ccg ggg ccc	480
Lys Ala Pro Ser Ala Ser Leu Pro Ser Pro Thr Arg Leu Pro Gly Pro	
145 150 155 160	
tcg gac acc ccg atc ctc cca caa ttt cct gat gga gag ttt aca atg	528
Ser Asp Thr Pro Ile Leu Pro Gln Phe Pro Asp Gly Glu Phe Thr Met	
165 170 175	
cag ggg tgc cca gaa tgc aag cta aag gaa aac aaa tac ttc tcc aag	576
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180 185 190	
ttg ggt gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca	624
Leu Gly Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala	
195 200 205	
tac ccc act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac	672
Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn	
210 215 220	
atc acc tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc	720
Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala	
225 230 235 240	
acg gta atg gga aat gcc aaa gtg gag aat cac aca gag tgc cac tgc	768
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ttcttttagc	tgaaaattag	ataaacctag	actcagtcca	tttctatcca	gaaaggaaat	240
gagataaatc	acaacctcat	ttcacagacc	taacggtcat	tggctcctta	gaggtagagt	300
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atgcaagcta	aaggaaaaca	aatacttctc	caagttgggt	gccccaatth	atcaatgcat	1020

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gcc cca att tat caa tgc atg ggc tgc tgc ttc tcc aga gca tac ccc	309
Ala Pro Ile Tyr Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro	
55 60 65	
act cca gca agg tcc aag aag aca atg ttg gtc cca aag aac atc acc	357
Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn Ile Thr	
70 75 80	
tca gaa gcc aca tgc tgt gtg gcc aaa gcc ttt acc aag gcc acg gta	405
Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala Thr Val	
85 90 95	
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Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys Ser Thr	
100 105 110	
tgc tat cac cac aag att atc gaa ggt cgt gac tac aag gac gat gac	501
Cys Tyr His His Lys Ile Ile Glu Gly Arg Asp Tyr Lys Asp Asp Asp	
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Asp Lys	

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 Tyr Pro Thr Pro Ala Arg Ser Lys Lys Thr Met Leu Val Pro Lys Asn
 65 70 75 80
 Ile Thr Ser Glu Ala Thr Cys Cys Val Ala Lys Ala Phe Thr Lys Ala
 85 90 95
 Thr Val Met Gly Asn Ala Lys Val Glu Asn His Thr Glu Cys His Cys
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 Asp Asp Asp Lys
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Cys Gly Gln Ala Met Ser Phe Cys Phe Pro Thr Glu Tyr Met Met His	
15 20 25 30	
gtc gaa agg aaa gag tgt gct tat tgc cta acc atc aac acc acc atc	144
Val Glu Arg Lys Glu Cys Ala Tyr Cys Leu Thr Ile Asn Thr Thr Ile	
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Cys Ala Gly Tyr Cys Met Thr Arg	
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Asp Ile Asn Gly Lys Leu Phe Leu	
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Pro Lys Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu	
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Tyr Lys Thr Val Glu Ile Pro Gly Cys Pro His His Val Thr Pro Tyr	
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Phe Ser Tyr Pro Val Ala Val Ser Cys Lys Cys Gly Lys Cys Asn Thr	
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gac tat agc gac tgc ata cat gag gcc atc aag aca aat gat tgt acc	802
Asp Tyr Ser Asp Cys Ile His Glu Ala Ile Lys Thr Asn Asp Cys Thr	
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Ser	Ser	Lys	Ala	Pro	Ser	Ala	Ser	Leu	Pro	Ser	Pro	Thr	Arg	Leu	Pro		
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ggg	ccc	tcg	gac	acc	ccg	atc	ctc	cca	caa	ttt	cct	gat	gga	gag	ttt		946
Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	Phe	Pro	Asp	Gly	Glu	Phe		
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aca	atg	cag	ggg	tgc	cca	gaa	tgc	aag	cta	aag	gaa	aac	aaa	tac	ttc		994
Thr	Met	Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe		
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Ser	Lys	Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser		
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Arg	Ala	Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro		
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Lys	Asn	Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr		
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Lys	Ala	Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys		
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cac	tgc	agc	act	tgc	tat	cac	cac	aag	att	atc	gaa	ggc	cgt	gac	tac		1234
His	Cys	Ser	Thr	Cys	Tyr	His	His	Lys	Ile	Ile	Glu	Gly	Arg	Asp	Tyr		
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 Gly Tyr Cys Met Thr Arg Asp Ile Asn Gly Lys Leu Phe Leu Pro Lys
 50 55 60
 Tyr Ala Leu Ser Gln Asp Val Cys Thr Tyr Arg Asp Phe Leu Tyr Lys
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Gln	Lys	Ser	Asp	Val	Val	Gly	Val	Ser	Ile	Gln	Asp	Ser	Ser	Ser	Ser
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Lys	Ala	Pro	Ser	Ala	Ser	Leu	Pro	Ser	Pro	Thr	Arg	Leu	Pro	Gly	Pro
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Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	Phe	Pro	Asp	Gly	Glu	Phe	Thr	Met
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Gln	Gly	Cys	Pro	Glu	Cys	Lys	Leu	Lys	Glu	Asn	Lys	Tyr	Phe	Ser	Lys
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Leu	Gly	Ala	Pro	Ile	Tyr	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala
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Tyr	Pro	Thr	Pro	Ala	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Pro	Lys	Asn
	210					215					220				
Ile	Thr	Ser	Glu	Ala	Thr	Cys	Cys	Val	Ala	Lys	Ala	Phe	Thr	Lys	Ala
225					230					235					240
Thr	Val	Met	Gly	Asn	Ala	Lys	Val	Glu	Asn	His	Thr	Glu	Cys	His	Cys
				245					250					255	
Ser	Thr	Cys	Tyr	His	His	Lys	Ile	Ile	Glu	Gly	Arg	Asp	Tyr	Lys	Asp
			260					265					270		
Asp	Asp	Asp	Lys												
		275													